score_list:					
Sequence	Strd Orig		EScore Len	i IIa	Documentation
pirl:GOHUT1	+ 2487.00		2.4e-158	455	! tumor necrosis factor receptor
pir2-J04302	+ 1738 On	2017 64	2.10.108	46.1	
piri:Gor:T1	+ 1563,50	INCH. 69	y.20.97	461	factor
Pirl·GOMST1	+ 1521 00	1817 91	6 30-94	454	! tumor necrosis factor receptor
pir2:154182	+ 290.00		8.0e-12	435	I tumor necrosis factor receptor
piri::QHPN	# 240 S0		1.60-08	4:7	' nerve growth factor receptor pd
pir1.A26421	. 223.00	264.18	2.40-07	425	! nerve growth factor receptor pr
pir2.838634	. 205.00	241.84	3.74.06	474	! tamer necresis factor redeptor
pir2::48854			1 00.06	45.9	! gene marine tumour necrosis fad
pir1.A35356	CU 102 +	240 P4	4.3- 06	46.1	I tumbr necrosis factor receptor
pirl:GQV2ML	00.00%		8.2e 06	326	: T2 protein - myxama zirus (stra
pir1:JN0006	+ 197.50		1.2e 05	416	! nerve growth factor receptor, 1
	192.03		2.8c.05	325	
pir2 A46484	. 191 50	35 835	3 J 05	327	! apoptosis mediating membraneras
pir2:JC2395	177.00	211 07	0 0000	45¥	Pas antigen precursor - rat
pir2:A4(m?h	+ 177,000	7 X = [7	11 (110):11 4	ر ۲	apoptosis-mediating surface and
pir2: A46476	+ 176.50	210 91	0 0003	305	! R rell-assoriated surface moled
pir2:F75518	175 50	202 37	7 JON 7	628	! hypothetical protein Deigocod
pir2.043674	168 %	73 361	010000	5	1 USA profesti human hermasystics
pir1:A46517	4 147,09	641.067	0.0013	097	2
pir2-A60771		_	0.0014	277	! M-cell activation protein CD40
piri.b72175	• 166 %	_	\$1,00°C	14.	1 GZR profein - variola minor vid
pirt:Tr8613		_	7 0021	¥ 7.	t hypothetical protein GDF vari
	+ 164 00	_	0.002]	10 10 10 10 10 10 10 10 10 10 10 10 10 1	i gene 448 protein - variola vird
pir2:A42086			0.0043	3' E' 3	1 CO30 antigen precursor hawan
pir2.042125		_	0.0042	677	I trophoroite eysteine riel surfa
pir2-714754		<u>ت</u> م	9.0048	066	: hypothetical protein DKFZp564F0
pir2:137383		7		314	! FAS soluble protein - human
pirl.QQRE3		×	0.0057	660	i BHI.Fl protein - human herpesvid
pir2:T09059	+ 156 50	17.4	0 0057	1964	noteh4 mouse
pir2:S29405			0.00%	r t	i glycoprotein 350/220 human hd
pir2.4372??	05 551 1	186 03	0 0077	294	i murin, tracheal (AMN 22) - homa
pir2:848423	+ 155.50	183.94	0.0075	392	! homeotic protein engrailed 1 -
pira:A43942	15 50	15.	13 12(1E, 5,	9.10 \$! nurin 2 precursor, intestinal
piti.ILL759	· 155.00	169.04	0.0071	41.81	! hypothetical protein FCCH12.3
pir2:88824			2 #.OU U	:: [:	(En,'Spm-like transposen protein
pir2-144768	152 50		0.0117	£0.7	! antifreeze glycopeptide APGP po
pir2:148141		177 37	กการค	163	! acrogranin guinca pig (fragmd
pir2:E70803	152.50	_	0.0114	456	~
pir1:00BE21	+ 152.50	174.27	0.0112	307	! membrane antigen gp350 human

A. Accessión, Si2057
A:Molecule Lype, aRNA
A. Residues, 19455 SNOPS
A. Cross reference, 1890; NRD 197223, FILE CARRODELL, FIS GRIDA
A. Cross reference, 1890; NRD 1974; Privier 1, Tr. 1974; Privier 1

3530 ' uncesventional myesin 19

pir2:A59266

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A, Pross referred 1, 28 MPRC24, Annual 200241, IllinaAARSELELL FLL. 1902445
E.Himmier, A., Maurel Foly, L., Kreenke, M., Schearlel, F., Fibermaier, K., Lantz, M. FNA Poll Biol, 9, 265-715, 1990
A,Fiber McLecular Clouds and expression of human and rat tomor necrosis factor rece
A,Relecence number, A36555; MOID:91090841
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A.Madouale Type, protein

A.Madouale Type, protein

A.Bresidous, 73-78,47 FT, X, 75-79, XX, 762-34, NR, 77X, 777-1047107-128; 161 167, X, 716

A.Mato, the putfied protein, called tumor nectosis factor binding protein, is a solution the putfied protein, K.; Chanty, D.; Turner, M.; Peldmann, M.

R.Cher, Nall, A.ad. Sea, 0.5.A. 87, 780-788, 1990

A.Title, Clearing of London Long Actions Lance (TME) receptor no NAR and expression of A.Reference number, A.8281, MUEL-91017509

A.Accession: A3828
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Unablactor receptor 1 precursor [validated] - human
Walternate names. PG tunor necrosis factor alpha fahibitor, IMF is epost type 1
NyContains; tunor necrosis factor alpha fahibitor, tunor necrosis factor binding prot
C.Species: Homo sapiens (man)
C.Data and Man 
          2187 | Lascent polypeptide-associa
439 | Childinase (ED 3.21.14) prec
755- | produce eto kinasc interact
312 | hypothetical protein (sdsB 7.
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A:Note: part of this sequence, including the amino cod of the mature protein, confirm
B:Schall, T. J., Lowis, M., Koller, K.J., Too, A., Elbe, G.C., Wong, G.H.W., Gatanaga,
Ccl. 61, 361-370, 1990
A:Title Modevial charing and expression of a receptor for human tumor necrosis fact
A:Reference number: A34900; Multi-90295288
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A/Reference number: A24899; MUID:50235284
A/Accession: A34899
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A)Cross references: GH M75964; GB:M75865, GB:M75866, NB:g339748, PDB:AAA61201.1: PJ
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A;Residues: 1-455 <LARS
A;Cross-references: GB:M58286; GB:M33480; NID:q339753; FIDN:AAA36753.1; PID:q339754
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A:Cross-references: GB.M63121; Nib:q329755, Firm.AA226754.1, Fir.q339756
A:Accession: C36555
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0.0143
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177.73
173.76
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          151.50
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3269-3278, 1990
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A, Rusidues, 1:455 <SCH>
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Cell 61, 351-359, 1990
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A,Residues: 1-455 <GRA>
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A,Residues, 1 455 kHPC
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A,Prosstrofero
          piri:13:0826
piri:551939
piri:86587
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A,Molecule type, protein
A;Peaidues 41 43, X',45 23, X',55.57 .SEC:
Proditationaga, T.; Hwang, C.; Kohr, W.; Cappuccini, F.; Lucci III, J.A.; Jeffes, E.W.B.; Le
Proditational Anada Sci II S.A. 87, 8781-8784, 1990
A;Title: Purification and characterization of an inhibitor (soluble tumor necrosis facto
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A;Molecule type: protein
A;Molecule 41 43,7X,45 53,7V,55.57,7XK,50 50LS/
A;Residues, 41 43,7X,45 53,7V,55.57,7XK,50 50LS/
A;Residuental source: renal failure patient urine
B;Engelmann, II., Novick, D., Wallach, D.
J. Biol. Chem. 265, 1531-1536, 1990
A;Tii.Let. Two Lunar nectosis, factor binding proteins purified from human urine. Evidence
A;Reference number: A35010; MUID:90110215
A;Accession: A35010
                                                                                                                                                                                         RiSeckinger, P.; Vey, E.; Turcatti, G.; Wingfield, P.; Dayer, J.M.
Eur. J. Immunol. 20, 1167-1174, 1990
Eur. J. Immunol. 20, 1167-1174, 1990
A.; Faritle. Tumor recrusis Lactor ishibiler: Furification. NH-2 terminal amine acid sequence A; Perference number: A60231; MOID:3022116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F)22-455/Product: Usmor necrosis factor receptor I #status predicted AMT.>
E)30-211/Domain extracellata #status predicted EXT.
E:41-201/Product: TNF binding protein I (tumor necrosis factor alpha inhibitor) #status
E:44-82/Domain NGF receptor repeat hymology +NCI.
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A;Residues: 41.45 / ENG.
A:Experimental source: normal urine
B:Rajhara, 7: Asada, A: Kirihara, S.; Kato, K.
Biosci, Biotechnol, Biochem. 58, 2225-2288, 1994
A;Title: Amino acid sequence of natural tumor necrosis factor alpha inhibitor purified
A;Reference number: JC2404; MUID:95128033
A/Title: Cloning and partial characterization of the promoter for the human p55 tumor A/Reference number: JT0758; MUID:94085779
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A;Map position: 12p13 2:12p13 2
A:introns: 13/3: 65/1: 108/1: 158/1: 184/2: 209/1; 247/1; 256/3: 343/1
C;Superfamily, tumor nectosis factor receptor type 1, NGF receptor repeat homology
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A;Residues: 41-53, X', 55-144, X', 146-150, 'X', 152-186, 'X', 188-201 -KA;
A;Experimental source: urine
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F)168-1967/Domain. NGF receptor repeat homology <NG4-
F)117-2-4/FOrmain. Frankmembrane #status predicted *NEN-
F)235-455/Domain. intracellular #status predicted <NT>
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A;Accession: A38258
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                                                                                                                     A: Molecule type: DNA
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51 GOTGITEGITGGGGAATATACOOPORGGGGTTATT GGACTGGTCCCTCACC 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACTIGITAAGAAAAGCITTGGAGGAAGTTGTGTGCTTGCTACICTAGATTGAG 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  601 AATGTTAAGGGCACTGAGGACTCAGGCACCACAGTGCTGTTGCCCCTGCT 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             651 CATITICITIGGICITIGCCITTALCCCTCCTCTTCALIGGITTAATGT 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                751 füdaüadüldaaaaagagggggagiltigaaggaartaitantraattaagggggt ggg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              801 GOTOTAAATOTAAGTTOTAGTGOTATTOTAGGTTOTAGGTTOTAGGTGGG 850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                851 GOTTCAGTCCCGTGCCCAGTCCACCTTCACCTCCAGCTCCACCTAIACC 900
                                                                                                                                                                                                                                                        101 TARRESAMENTARRESAMENTARIA TRACTIGITATION CONTACTABATATATO 150
                                                                                                                                                                                                                                                                                                                                                           151 CACCCICAAAATAATICGATTIGCIGTACCAAGIGCCACAAAGGAACCIA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               167 ICYSHISALadlyPhePheLeuArgGluAsnGluCysValSerCysSerA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             251 SerThrProGluLycGluGlyGluLeuGluGlyThrThrThrLysProLe 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              267 uAlarreAsniroSerPheSerProThrProCl7PheThrProThrLeuG 284
                                                                                                                                                                                                                                                                                34 euGlyAspArgGluLysArgAspSerValCysFroGlnGlyLysTyrIle 50
                                                                                                                                                                                                                                                                                                                                                                                        17 uLcuLcuValClyIlcTyrProSerClyValIlcOlyLcuValProHisL 34
                                                                                                  1 MetGlyLeuSerThrValProAspLeuLeuLeuProLeuValLeuLeuGl 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ATGGGCCTTCTCCACCGTGCCTGACTGCTGCCACTGGTGGTTGCTTGGT
                                                                                                                                                                             Align seg 1/1 to: GQHUT1 from: 1 to. 455
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284 lyPheSerProValProSerSerThrPheThrSerSerThrIyrThr 300

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A:Fitle: Cloning of the cDNA encoding the porcine p55 tumor nectosis factor receptor.
A:Reference number: JC4302; MUID:96011645
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tumor necrosis factor receptor p55 precursor - pig
C.Species. Sus serorfa domestica (domestic pig)
C.Date: 29-70-1995 #sequence_revision 08-Peb-1996 #text_change 23-Jul-1999
C.Accession: JC4302, PC4093
R.Suter, B.; Pauli, U.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A.Cross-references GB.819994, NED.41141752, PERN.AAC4849911, PER.41141753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1101 CCCGIIGCGCIGGAAGGAATICGIGCGGCGCTAGGGCIGAGCGAAAAA 1150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1251 GCIGGAGCIGGIGGGAGAGGGGGGAGAGAAAAAAGAGGAAAGTGGAGAGAGAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  951 CIATCAGGGGGTGACCCATCCTTGCGACAGCCTCGGCTCCGACCCCA 1000
367 OProLeuArgTrpLysGluPheValArgArgLeuGlyLeuSerAspHisG 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              384 luIleAspArgLeuGluLeuGlnAsnGlyArgCysLeuArgGluAlaGln 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 ProGlyAspCysProAsnPheAlaAlaProArgArgGluValAlaProPr 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: protein
A;Residues: 1-7 <802>
A;Experimental source: kidney cell line 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-461 <SUT>
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301 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGAICTCTTGTTG 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 451 AATGGGACGTGCACCTCTCCTGCCAGAAAAACAGAAACACGTGTGCAC 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      651 CALLLECT FOOT THE GATTEL HANDS FOR LECAL DISTRIBATED 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         151 CACCLICAAAATAALICGALILGGIGIAC AAGIGCOAGAAAGGAACTA 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  201 CHICHACAAHGAMMGJOCAGGGGGGGGAAGAAAGGAAMGGAAHAGAAGAAHAAGAAHAAGAAHAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          251 GIGAGAGGGGGGGGTTCACCGTTCAGAAAACCACCICAGACACIGCCIC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101 SerCysSerLysCysArgSerGluMetSerGlnValGlnileSerProCy 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       351 CACACTGCACCGGACACCCTGTGTGGCTGCAGGAACAACAATACGGC 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 184 SDCYSLYSASDADA ASPCYSTYSASD COCYSPICA, albrsordin 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60i ANIGIIAAGOGACIGAGGACICAGGA PAGAGIGIIGIGGIGIIGGA 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           200 ThrArgAshAspPheGlnAspThrClyThrThrVaiLeuLeuProLeuVa 216
                                                                                                                                                                                                                                                                                                             51 GC1711GC1GGAATATAGGGGTFAGGGGTTATTGGAGTGTFGFCTCAGT 10U
                                                                                                                                                                                                                                                                                                                                                                                                  101 TAGGGGACAGGGAGAGAGATAGIGTGTGTCTTAAGGAAAAIAIATT 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    151 AshClythrValGInbeuProCysLenGlubysGInAspThrtHeGysAs 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         167 nCysHisSerGlyPhePheLeuArgAspLysGluCysValSerCysValA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    751 TOSMIND LOADAMASAGGGAGTTGANGGARGIACIAAAGGGGT 798
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                                                                                                                                                                      Align seg 1/1 to: 274392 from: 1 to: 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality: 1738.00
Ratio: 4.526
                                                                                                      alignment_block:
US-09-525-998A-1 x J24302
alignment_scores:
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P;30-201/Product: tumor necrosis factor binding protein #status predicted <IHP> <math>F,44-82/Comain: NGF receptor repeat homology <NG1> <math>F;84-126/Domain: NGF receptor repeat homology <NG2>
                                                                                                                                                                                                                          F;54,151,201/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51 CCTCTTGCTGGGAATATATACCGGGTTATTTGGACTGGTGTTGACT 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84 ysAsplysGlyThrPheThrAlaSerGlnAsnHisValArgGlnCysLeu 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTG 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           351 CACACTOGACACACOCOTOTOTOCOTOCAGGAGGAAGAACAGTACCGG 400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            501 CTGCCATGCAGGTTTCTTTCTTAAGAGAAAACGAGTGTGTCTCCTGTAGTA 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            551 ACTGIAAGAAAGCCTGGAGTGCACGAAGTTGTGCCCIACCCAGATTGAG 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     184 isCystystysAsnClnCluCysMetLysLeuCysLeuProProValAla 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34 euGlyAspArgCluLysArgAspAsnLeuCysProGlnGiyLysTyrAla 50
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                                                                                                                                                                                                                                                                                                                                                                                           Pario: 4.203 Gaps: 4
Percent Similarity: 82.119 Percent (destity: 64.901
                                                                                          P.127 187/Phomain NGF receptor repeat homology (NG3)
P.168-204/Pomain: NGF receptor repeat homology (NG4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: GQRTT1 from: 1 to: 461
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Ratio: 4.203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
US-09-525-998A-1 x GQRTT1
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C:Comment: This protein is one of two known receptors for both TNF-alpha (eachectin) and
C:Superfamily: Tumor necrosis factor receptor type 1; NNF receptor repeat homogony
C:Keywords: duplication; qlycoprotein: receptor: transmembrane protein
F:L20/Domain: signal sequence #status prodeicted serve
F:30-461/Product: tumor necrosis factor receptor type 1 #status predicted sMATS
F:30-707,250main. extracellular #status prodicted serve.
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A;Accession: B36555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A : Mauror-Fogg, I : Kroenke, M.; Scheurich, P.; Pfizenmaior, K.; Lantz, M.; iol. 9, 705-715, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C:Species: Rattus norvealous (Norway rat)
C:Date: 30-Tun-1992 #MPT:PETE_FRYICION 07-0ct:1994 #text_charge 21-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tumor necrosis factor receptor | precursor - rat
N;Contains: tumor necrosis factor binding protein 1 (TNP blocking factor)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1130 GCCTAGGGCTTGACCTACCACTATGGATGGGCTGGAGGGGGG 1179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 848 TGGG/TTP?AGTQPQGTGAGTTPGAGCTTCAGCTGCAGCTAT 897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        316 eAlaProProClnGlyAlaGlyProlleLeuProMetProProAlaS 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              400 ArgCysLeuArgCluAlaCinTyrSerMetLeuAlaCluTrpArgArgAr 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          433 spMetAspLeuLeuGlyCysLeuGluAspIleGluGluAlaLeuArqGly 449
266 rphoglyproflowhribarbaserprofloproserphoserproflar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            283 hrThiPheserProValProserPheserProlleSerSerProInrPne
                                                                                                                                                                                                                                                                                                                                                      942 GGCACCCACCCTATCAGGGGGCTGACCCCATCCTTGCGACAGGCCTCGCCT
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A; Residues: 1-461 <HIM>
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CiSpecies: Mis musculus (house mouse)
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                                                                                                                                                                                                                                                                   234 ysArgTyrPrcClnTrpArgPrcArgValTyrSerIleIlcCysArgAst
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A;Molecule type: mRNA
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A,Grass references, 3:1M60468, Nin.4D99825, Fir.M.AAA147..., Fir.Gopeland, N.S.: 3
RiGoodwin, R.G.: Anderson, D.: Jerzy, R.: Davis, F.: Brannan, C.I.: Copeland, N.S.: 3
Woll, Cell, Biol, II, 3200-3265, 1991
A.E.: Molecular cloning and expression of the type 1 and type 2 murine receptors 1
A,Eatrense, number, Afolfs, Molocofiles
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ArReference number: 14432; Muldo:94245292
ArRecession: 154532
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PyPothe, J.G.; HUPATHIRAN, H.; Gentz, R.; Ecsslader, W.; Steinmetz, M.;
Mol. Immunol. 30, 165-176, 1993
Aziitle: Genomic organization and premoter function of the mornine tumor nectosis fact
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RIBATTOLL, F. Taylor Fishwick, D.A.: Cope, A.P.: Kinschorthis, A.M.: Gray, P.W.; Fel-
Bur, J. Bamunol, 21, 1409-1455, 194
ALILLO Cloning, expression and cross linking analysis of the murine p55 tumor necto.
A.Reference number: $16677; MOLD:91285014
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A.Gross-reference: CREMT6456, MILLIDELETT FIRM.AAA10465.1. FIRGGELIDE
G.Comment: This protein is one of two distantly related receptors for both INF-alpha
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F.236-454/Domain: intracellular #status predicted FINI.
F.54.151,202/Binding site: carbohydrate (Asn) (covalent) #status predicted
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A.C.Cose-references: EMELIXE7796, NILLIGETRAB, FILANCAA40946.11: PIDIG54849
R.Bebo, B.F.
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A.Accession: 157826
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A;Residues: 1-454 <R01.
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ArResidues: 1-454 + LEW-
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A:Molecule type: mENA
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1 ATGGGGGTGTGCAGGTGGTGAGGTGCTGTTGGCAGTGGTGCTGGA

17	100 34	150 50	200	250	300	350	400 134	450 150	500	550	597	217	697 234	747	797	841 280	891 296	645
		DOGRAFAGGAGAGAGATAGTGGGGGGGGGGGGGGGGGGGGGG	CACCETCAAAA AATTOGATTTTGCTGTACCAAGTGCCACAAAGGAACCTA 	**************************************	agogo iggticaoggetigadaaacod ::: :::	AQCTGCTCCAAATGCCGAAAGGAAATGGCTCAGGTGGAGATCTCTTGTTG 	CACAGTGGACGGGGCGTGGGGGGCGCAGGAAGAACAGTACCGGC ::: :::	WFGGAOTGAAAACCTTTFCAGLOCTTCAATFGAAGCT 	AATGGGACGTGCACCTCTGCTGCCAGAGAAACAGAACACCGTGTGCACTTTTTTTT	CTGCCATGCAGGTTTCTAAGAGAAAACGAGTGTGTCTCCTGTAGTA :	TRACAAAAOOOTOOAAOAAAAATOOOOTA 	ARDETAADDOADERAGGAERAADAAAAAAAAAAAAAAAAAAAAAAAAAAA	IIIIAIGCECETCITC [[]][][];:::::[][culcaserheilethe	TOCAAGCTCTACTCCATT 	IOGACACCTISAAAAGAGGGGAGCTTGAAGGACTACT :::HI	GCTTCAGICCCACICCA [[I][[]][]] JaPheserProThrSer	g y	ACCTATACCCCCGTGACTGTCTC AACTTTTGGGGTTGTCTCTCTCTCTCTCTCTCTCTCTCTC
_	51	101 3 4	151	201 67	251 84	301 101	351	401 134	451	501 167	551 184	598 201	648 217	698 244	748	798	842 280	892

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Ribbachs, M.; Chaifanet, M.; Cassiman, J.J.; Van den Berghe, H.; Marynen, P. Genomics 16, 214-218, 1993
Aritic: Construction and evaluation of a hecoma library of human 12p transcribed seq A.Reference number, 154182, MUID.93252381
A.Recession: 154182
A.Status: preliminary: translated from GB/EMBI/DDBJ
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C.Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tumor necrosis factor receptor 2-related protein - human
Cispecies, Homo sapiens (man)
Cibato. 24 May 1996 #sequence_revision 21 May 1996 #text_change 17 Mar 2000
CiAccession: IS4182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule Lype: mRNA
A;Residues: 1-435 <RES>
A;Cross:references: GB:L04270, NED.4339761; PIDN:AAA36757.1; PID:9339762
                                                                                                                                                                     983 CCCTCCTCCGACCCCAFCCCCACCCCTTCAGAAGTGGGACGACAGC 1032
                                                                                                                                                                                                                                                                                                                                                                                          1083 CGIGGIGGAAAAAAGIGGCCCCTGGAAAGAAAITCGGGGGGGC 1132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1133 PAGGGCPGAGGACCACCACGAGATCGATCGGCTGGGAGGCTGCAGACGGGCGCC 1182
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                                                                                                                                                                                                                                                                                1033 GOCCACAGAGCACAGAGCTAGACACTGATGACCCCGCGACGCTGTACGC 1082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1183 IGCCIGCGCGAGGCGAATAMACATGGTGGCGACCIGGAGCGGCGCACC 1232
                                                                                     329 orLoufysSorValProAlaProThrSerValGlaLySTrpGlaAspSer 345
                                                                                                                                                                                                                                                                                                                                     346 AlaHis...ProGlnArgProAspAsnAlaAspLeuAlaIleLeuTyrAl 361
                                                                                                                                                                                                                                                                                                                                                                                                                           378 etGlyLeuSerGluHisGluIleGluArgLeuGluMetGlnAsnGlyArg 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         297 ProlleSerProllePheGlyProSerAsnTrpHisPheMetProProVa 313
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A;Cross-references: GDB:1230195; OMIM:600979
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Quality: 290.00
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4	AlathrSerAlaProClyLeuAlaTrpClyProLeuValLeu.ClyLeuP 22	61
83	TTGGACTGGTC)5
0.00	GACAGGAGAAG, AGAGATGTG G G GCCAAGGAAATATATCA 15 FILLIFIER FILLIFIE	, 25
53	OCCICAAAAIAAITGAATITAATGIAAGAAAAAAAAAAAAA	1 0 8 2 2
03	TOTACAATGACTGTCCAGGCCGGGGGGGAATAAGGGACTGCAGGGGGGGG	- ಆ ೯
25.3 84	GAGAGCGGCTCCITCACGCTTCAGAAAACCACCCCAGACAGCGCTCAG 302 ::::::)2)0
0.0	CIGCICCAAAIGCGAAAGSAAAIAGGICAGGGAGAAICICIICIIGGA 352 	52
153	CASIGRAPPOSSAPAPOSIGIGIOS TROPOSARANO ASTAROS GONT 40 11)2 33
34	TAFIGGAGTGAAAAGCTTTTCCAGIGCTTCAATTGCAGCCTC44	14
4.5	TGCCICAALGGGAPTGLGCAPTTCTCTTCCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	87 64
88 64	ACACGGGGGCGC1GCCAIGCAGGIICCIICIAGAGAAAACGAG 53 :::	34
35.	TGTGTCTCCTGTAGTAACAAAAGCCTGGAGTGCAGGAGTTGTG 58	34 95
985	35 CCTACOCCAGATIGAGAALGIIAAAGGGAUTGAGGAUTCAGGUACCACA. 63 [1] [1]	33 10
333	633	33
10	ystysAsnProteuGluProfeuProProGluMerSerGlyTtrMetLeu 22	نو
34		74 40
575 240	ATCOSTOSTICATIONITIANIGIALOGOTACOANOGIGGAAGICC, 72 [1:1: 1:1] [1] [1] [1] [1] [1] [1] [1] [1] [1] [23
24	isPreserteatyanitysteritySertaule:	96 53
57	'57 ccrdaaaaadaddddagcrrdaagdaacracraadccccrgdgccc 806 Hitti: HIHH 266 Prodinglyglufiy Pr 271)6 7.1
307	AAACCA AGCIICAGICCANIGAGGGIICAGCC 84 [11

ProAspLeuValGluProLeuLeuLeuLeserGlyAspValSerProVa 304	IRCAGCII MAGNICCAGGICCANTALANDOGONOSII GACIISTONAANTI 920 	HOGOGODO COGOMAGAGO GO O CONTROLA CONTRA CON	FOCTIGOSACAGOCTINGOCTONSACOMALOSOCAA 1007 FEBSE F	1007	isGlyThrAsnOlyTleHisValthrGlyGlySerMetthrHedlyThr359	-	AsnileTyrileTyrAsnGlyProValLeuGlyGlyProProGlyPro 375	GGAGGAAGAGAAAAAGAGAAAGAAAAGAAGAAGGAAAA 1971 	ACGC1GTACTCCTGGTGGAGAACGTGCCCCGTTC YCTGGAAGGAALF 1121 FILLTT Profitobrotheliadase 343	OBTECTOR CTRACECT LANCOACTAC GAST CALCED TO COME THE TITLE TO THE TENT OF THE	PTOVERY FOR FOUR PRODUCTION OF THE PTOTEST CONTINUED TO SERVICE TO	AGGCGGGAANGCGAGGCGGAGGCGAAGGTGATTGGGAGG 1268 	1283 429		ica attinit, [calidated] laman Mar gam atort_change Marigore California Action Action	Cell 47, 945-584, 1946 A:Yitle: Expression and structure of the human NSF receptor A:Reterence number, A2521H, MID:87051725		\$150.4183±05	d. min. mailter off. off. off. Strattenan, G.J. Hompson, S.J. 6780. 27, 1987. d amino terminal sequencing of homan melanoma nerve growth ta	64: M0110: 8708#574	Asmosecute Type: Footein Askresinges: 99-317 (1733-427 Triv.45-46, 1875-51, 1887-54-56 KMAR) Astronomiana association inclinations (1731-170) in the APPS
ProAspLeuValGluPro	TCCACCTTCACCTCCAGGE TTTTTT 	TGCGGCDD CCGGAGAGAC ::: ITT ::: InGInSerProLeuAsp.	HOCHGGGACAGGCTHGC Tites: Tites:		isGlyThrAsnOlylleH		Asn HeTyr HeTyrAsn(GGGAGGATAGPGCPTATAR ::: : GlyAspLetProAld	ACGC1 G1 ACGC3C1 GG1 G	0616066.017666010 ::::	ProofigirioProcificas ACAAGGGGGGGTGGGTGGG	ACCCCCCCANDCCOCCCC ::III	CGTGCTCCGCGACAT 128 ::: :: ArgGlyProArgAsh 429	seg_name: pirl:GwHWN	seq_documentation_block: Let or time(List) : the reful prediction: C.Species: Home sapiens (mar) C.Date: 31 mar-1988 #sequence_review: C.Arcessin: Action of the recovered of the resident	545-554, 1986 Expression and struce number: A25218,	on: A252:8 e type: mKNA	8: 1:427 - JOH> Fleren en SE.M.476 N - Diotagnation (hem. 48, 225-232, Purification and and	A)Reference number: A60204; A;Accession: A60204 A:Molecule tyme: co.tein	e Type: procesu s: 29-31,11,33-42, cntal source: melar
842	304	921	971	1007	343			1022 (376	1.0721 1.82	394		1222 / 408 /	1269 0	seq_name:	seq_docum LELV 1155 N;Alternal C;Species C;Date: 3 C;Arcessi	Cell 47, Armitic: I	A; Molecule	A;Residue A;Clossit D:Maxono	J. Neuroci Ayfritle: J	A; Referen A; Accessio	A) MOLECALD A) Residues A) Experime

78 erAlaThrGluProCvsIvsProCvcThrGluCvs A:Note: this sequence has been corrected by a note added in proof to follow the nucleotic Rivissava) hala. P.: Lescyk, J.D.: Lin Goerke, J.: Ross, A.H.
Arch. Hiodone. Biophys. 294, 244-25, 1992
A:Title: Structural domains of the extracellular domain of human nerve growth factor red A:Reference number: \$21689; MUIS:92198017
A:Reference number: \$21689; MUIS:92198017
A:Reference number: \$21689; MUIS:92198017
A:Residues: Preliminary
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R:Residues: Preliminary: translated from CB/EMH:/DDE:
A:Residues: Preliminary: translated from CB/EMH:/DDE:
A:Residues: Preliminary: translated from CB/EMH:/DDE:
A:Residues: Telerences: GB:RE152: NID:9189206; PIDN:AAA36363.1; PID:9189207
C:Comment: This receptor in the extracellular domain may form part or all of C:Comment: This receptor in the extracellular domain may form part or all of C:Comment: This receptor undergoes both N- and O-linked glycosylation. Cisupertamily: merve growth factor receptor. NGF receptor repeat hamology Ciscoverds, duplication, glycoprotein, heterodimer, monomer, phosphoprofein, receptor, File28/Domain: signal sequence #status predicted <2000 File28/Domain: signal sequence #status predicted <2000 File2 for prediction received to the Latter septor #status experimental SMAT. File2 for prediction = Artsechlor #status redicted = EXT. File2-65/Domain: NGF receptor repeat homology <NGI> F.273-4272/Domain: trinsmontrano #status predicted <TPM>
F.273-427/Domain: intracellular #status predicted <INT>
F.560/Rinding site: carbobydrate (Asn) (covalent) #status predicted 234 TACGGACTGCAGGGAGTGT GAGAGGGCTCTTCACGCTTCAGAAA 280 184 IGCCACAAAGGAACCIACTIGIATAATGACTGTGTGTGGGGGGA 233 134 CCCAAGGAAAATATATCCACCCCCAAAATAATTCGATTTGGTGTACCAAG 183 34 CCACTGGTGCTGGTGGTTGTTTGGTGGAATTATTAGGTGAGGGTTTATT 83 13 ProArgLeuLeuLeuLeuLeuLeuLeuGlyValSerLeuGlyGlyAla.. 28 ..SerGlyGluCySCysLysAla 46 47 CysAsnLeuGlyGluGlyValAluGlnProCys...GlyAlaAsnGln.. 61 62 ThrValCysCluProCysLeuAspSerValThrPheSerAspValValS 78 240.50 Length: 487 1.108 Gaps: 25 44 559 Porocot (doutlity: 22,819 Filow-147/Pownyie, McF receptor Meport bomology MG3> Filos-189/Domain, MGF teceptor repeat bomology sMG4> Filos-248/Region: serine/threonine-rich A.Gene: GDB:NGFR A.Cross-references: GDB:120234; OMIM:162010 Align seg 1/1 to: GQHUN from: 1 to: 427 __ 33 roThrelyLeuTyrThrHis A:Map position: 17q21-17q22 US-09-525-998A-1 x GOHUN Quality: Ratio: Percent Similarity. aliqnment_scores:

C,Geneties:

alignment_block:

281 ACCACCTCAGACACTGCCTCAGCTGCTCCAAATGCCGAAAAGGAAATGGGT 330

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331	CAGGITGGAGATTTTTTTTTTTTTTTTTTTTTTTTTTTTT	377
3.5	GluAlaAspAspAlaValCys	108
	8 CTSTANDARANTANTANTANTANTANTANTANTANTANANTAN	C1 C
-	richaspioning in gar	
128	GPT310AATTGCAQQQTGC9QQTQAARQQQAQQCTCTGCTGC 	474
ï		201
· ·	OlucysProAspGlyThrTyrs	
٠. د	AAGAGAA AACGAGTGTGTCTCTCTAGTGT	n.
۲. ۲.	::: ::: :::	:72
556	AGIPTGT130CTACCCCAGAT	597
172		188
a. G	ACCACAG EGCTGT EGC	647
189	ulleProC!Y	193
648	CCTCCTCTTCATTGGTTT	269
193		193
3.5	STA LEGEPTAÇEAAÇĞEPTIĞAAĞTIÇEAAĞETETACTECATTETITLETĞE	747
194	Argirp	198
748	AATICJACACCI GAAAAAGAGGGGGGGCTTGAAGGAACTACTACTAAGC	797
199	SerThrProProGluGlySerAspSerThrAlaProSerThrGluBr	215
798	CCTGGCCCTAAACCTAAGC TTCAGTCCCAACTCCAGCTTCA	838
215		232
839	CCCCCACCTICACTICACTICACTICACTICACTICACCTICACCTICACT	888
232	alThrThrValMetGlySerSerGlnProValValThrArgGlyThrThr	248
889	TCCACCTATACCTCTCGTPGACTGTCCCAACTTTTGGGCCTTTTTTTTTT	427
249	AspAsmiculloProValTyrCysSerlloLcuAlaAlaValValC!	265
928	CCCGGCAGAGGTGGCACCACCT	952
2.55	TlouValAla@TrileAlaPbel.ysArgTrpAsnScrCyslysClrAsnl.	C 8 C
953	ATCAGGGGGTTGAP CCCATTCTTTGGGGGGTTGGCTTGGAP	955
282	ysGlnGlyAlaAsnSerArqProValAsnGluThr	293
647	COCAUCICCAACICCCTTTCAGAAGTGGGAAGG GCCCACAA	1040
294	ProproprogludiyGluiysLeuHisSerAspSerGlyIleSerValAs	310
310	GCCALAGAGCT AGACACTGATGACCCGCGACGCTGTACGCC	1083
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307		011
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# Hydnment_block: US-09-525-998A-1 x A24431 Align seq 1/1 to: A26431 from: 1 40 GIGCTCGIGSAGIGITGGIGGAAIAL. :::IIIII	140 GAAAATATATA ACCOUCAAAAIAAIIC 11	receptor.	4 14 14 15 15 15 15 15 15 15 15 15 15 15 15 15		0.54 THOUTHOSTICHTOCHTHATOCHTO 1.94
1111	1216 ACCTOGAGONGANACANACANACANACANACANACANACANACANACAN	<pre>seq_name: pirl:A26431 seq_documentation_block: nerve growth factor receptor netre growth factor receptor is secies. Rattus norvegicus (Norvay rat) c; Species. Rattus norvegicus c; Species. Rattus norvegicus c; Species. Rattus c; Species. c; Species. Rattus c; Species. c; Sp</pre>	Asherocasion: A26431 Asherocale Lype: mKMA Asherolade Lype: KAD> Asherolade Lype: MKMA Asherolade Lype: Lype: MKMA Asherolade Lype:	C.Comment: This receptor is rand on sensory and sympathetic heurous, on neuroblastoma of C.Comment: The cysteinerich region of the extracellular domain may form part or all of C.Comment: This protein is thought to form a high-affinity receptor when it associates we Genetics: A.Introns: 20/3 C.Soperfamily, nerve growth factor receptor, NGF receptor repeat homology C.Koywords: duplication, glycoplotein, heterodimer, monomer, phosphoprotein, receptor; t F.1-29/thomain: signal sequence actains predicted A.S.C. F.30-425/Product: merve growth factor receptor #stalus predicted AMAT>	Fig. 955/25cmain. extracellain Fotatus predicted CEXIS (F. 87.66/20cmain. NCF receptor repeat homelosy CNGIS (F. 86-109/20cmain. NCF receptor repeat homelosy CNGIS (F. 81.00-109/20cmain. NCF receptor repeat homelosy CNGIS (F. 81.00-109/20cmain. NCF receptor repeat homelosy CNGIS (F. 81.00-109/20cmain. NCF receptor repeat homelosy CNGIS (F. 92-249/Reqion. serine/threonine-rich Action (F. 93-279/20cmain. transmemberose mainter predicted CNGIS (CNCINC)

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AGAGATAGTGTGTGCCCAAG 139
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PysthrValCysGiuAspfhrG 175
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pAlaAspAlaGluCysGluGlu 191
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                                                                                                 erserGlySlyAla.....29
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ACCOUNTAGESTALLALLEGGACT 89
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A; Molecule type: mRNA

995 22 1996-1948-1948-1948-1948-1948-1948-1948-1948
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A. Pross references: GR:MK0460, NID-gl99827; PiDN:AAA39752.1; PiD:gl99228
F.Kissencrghis, M. Fellowes, F., Feldenn, M., Chernajevsky, F.
submitted to the RMM. Data Library, May 1995
A.Description: Characterization of the promoter region of the murine p75 TMF receptor
A.Reference number: S54816
                                                                                                                                                                                                                                                                                                                        A.Residues: 1.22 -KKIS>
A.Crosa-references: EMBLX87.28, NID-4809043, FIDN.CAA60618.1; PID:q809044
A.Crosa-references: EMBLX87.28, NID-4809043, FIDN.CAA60618.1; PID:q809044
C.Supertamily: tumer necrosis factor receptor type 2; NGF receptor repeat homoloay; C.Supertamily: repeat homoloay redicted sign.
F.1 22/Domain: signal sequence #status predicted sign.
F.2 444,770-back. Lumon necrosis factor receptor type 2 #status predicted cMAI>-
F.40 77/Domain: NGF receptor repeat homoloay -NGI>-
F.74-120/Pomain: NGF receptor repeat homoloay -NGI>-
F.74-120/Pomain: NGF receptor repeat homoloay -NGI>-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    230 AGGATACGGACTGCAGGGAGTGTGAGAGCGGCTGCTTCAGGA 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         327 (GGGT) AGGT GARATCT CTT (TTT) TEG ACACTGGGACACACTGTGTG 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120 laCysGluAlaGlyArgTyrCysAlaLeuLysThrHis.....SerGly 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          415 AACCITIICCAGIGCIICAA1IGCAGCCICTGCCICAAIGGG...ACCGI 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                135 SerCysArgClnCysMetArgLeuSerLysCysClyProGlyPhcClyVa 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         462 GCACCICICICIGCOAGGAGAACAGAACACCGIGIGC...ACCIGCCAIG 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           151 lAlaSerSerArgAlaFroAsnGlyAsnValLeuCysLysAlaCysAlaP 168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          168 rodlyThrPhe....SerAspThrThrSerSerThrAspValCysArg 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   559 AAAA99216GGAGIGGAASIIGIGGGGTIAGGGAATTGAGAATGTAA 608
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          280 AANTENTINAANTIGOTIOASITGO...IOGAAATGOGGAAAAGAAAT 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89 AshCirPheArgThrCysLeuSerCysSerSerSerCysThrThrAsp., 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56 alystysFroFroGlyGlnTyrValLysBisFhedys...AsnLysThrS 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40 CysClnflcSerCinGluTyrTyrAspArgLysAlaCinMetCysCysAi 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity: 50.000 Percent Identity: 26.378
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A; Pesidues: 1-474 <600>
                                                                                                                                                                                                                                                       A;Status: preliminary
A;Molecule type: DNA
A,Residues: 1 22 <KiS>
                                                                                                                                                                                                                A;Accession: S54816
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pAlaValCysAlaProGluSerProThrLeuSerAlaIleProArgThrL 21	105 lacysGtwAlaclyArdtyrcysAlaLeutysThriffsser35 119
ZIB GUTYTVAL	120 SerCysArdInOysMetArdLeuSerLysCysClyProdlyPhedlyVa 136
	462 GCACCICTCTGCCAGAGAAACAGAAACACGIGTGCACCTGCCATG 508
753 GACACCEGAAAAAGAGGGGAGCTTGAAGGAACTACTAMAAGCCCTGG 802 HTHTH	CAGGITTCTTTCTAAGAAAAACGAGTGTGTCTCTGTAGTAACTGTAAG
803 CCCAAACCAAAGTTCAGTGCAGGTTCACCCCAACCTGGGG 852 :::[11:::	AAAAGCTOGACTOTACAAGTTOTACCCTTTTACAGTTOTACAGTTOTACCCTTOTACCTTOTACCTTOTACCCTTTTTTTTTT
853 TTCAGICCCGTG 864	198 Promisard: PrysseritetenAtalleProfiyAsiAlaSeritida (84
pir2:148854	184 pAlaValCysAlaProGluSetProThrteuSerAlalleProArathrt. 201
seq_documentation_block: qene murine tumour necrosis lactor receptor 2 protein · mouse (fraqment)	592
C.Spectes: Mus musculus (house mouse) C.Date: 02-101-1996 #sequence_revision 02-101-1996 #text_change 23 Jul-1999 C.Accession: 148854 D.Dowell F.E. Wilder (G. Determan (F. mada (A.))	AAGUGCACTAABACTTA
Arithe: Allelic variation of the type 2 tumor necrosis factor receptor yene.	218 ProdryproseroiningProseriateLendingSPredenstySeringEr 244
A; Reference number: 14884; MUID:95178848 A; Accession: 14884	2.5
A.Scara: profinitionary, utansfaced from CAYEMBLYDBAD A.Residues: 1-459 <res> A.Cross-references: EMBL:X76401: NID:q433830; PIDN:CAA53981.1; PID:q433831</res>	656 ICITIGGICITIGGCTITIATCCCTCCTCALIGGILIAAIGTATCGC 705 ::
Cosuperianty camer measures target by 177 Type 2. Not recited topical behalogy Existing NOF receptor repeat homology <nof></nof>	706 TACCAACGGIGGAAGTCCAAGGICTACIOCATIGITGTGGAAAATCGAC 755 ::: ::: ::: ::: ::: ::: ::: ::: 266 ::::::
digdment_scores: Quality: 204.50	756 ACCIGAAAANAAGGGGGGAACIIGAAGGAACIACIACIAAGGCCU 805
aliqnment_block: US-09-525-998A-1 x I48854	CAAACCCAAGCCCAACCCAAGGCTCACCCCCCACCCTGGGCTCC
Align seg 1/1 to. 148854 from 1 to. 459	roasportussereinaspalavaleiyteuolueineiniisteuteu
130 TGTCCCCAAGGAAATTAICCACCTCAAAATAATTCGATTTGCTGTAC 179 	856 AGTCCGGGCCAGTTCCACCTCCAGCTCCAGCTATACCC 902 ::: ::'TTTHITTT::::::TTTHITTT::::: 307 ThTThtAlaPioSerSerSerSerSerLougluSerSerAlaSerAl 323
180 CAAGIGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCGGGGC 229 :IIIII	903 GGGIGACIGTOCCAACITIGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
240 AWAATAYWAATGCAGGAGTGTGAGAAGGGTTCATCATCAGAA 279 ::11111 11 :::1111 ::::: 57 erAspThrValCysAlaAspcysGluAlaScMetlyTthrGlnValTrp 73	947 CACCITAICAN-MAGGA DARCHINSGANAMACHTNAGATON 995 HTTLESTEEL HTTLESTEEL HTTLESTEEN HTTL
280 AACCACCTCAGACACTGCTCAGCTGCTCCAAATGCCGAAAGGAAAT 326 	seq_name: pirl:A353% seq_donumentation_block:
	N.Alternate names 75k tumor nerosis lactor recopic; INF prospicr type 2 C;Species: Homo sapions (man) C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 68-bee 2000
90 - Ginvaldinihargalagyehariyschucimasnargvaloga 377 GCTGCAGGAAGAACGAGTAC	C) Acrossion, 4,5225, A.8617, A48416, A.4507, A2344, B.85436, 1,6694 R.Smith, C.A., Pavis, T., Anderson, D., Solam, L.: Beckmann, M.P.: Jerzy, R.; Dower, Reserve 248, 1019-1023, 1940

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GCTCTCCTGCCAGGAGAACAGAAACACGTGTGC...ACCTGCCATG 508
                                                                                                                                                                                                                                                                             aSerSerArgAlairoAsuGlyAsuVail.co/fysiysAla@ysAlair 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              clleGlatinSerThrlysGlyGlylleSerLeaProlieGlyleul 251
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                                                                                           CITTTCAGIGCT CAAT BCAGCCLCTCCALCSS...ARCGT 461
                                                                                                                                                   CysAruGinCysMetAruLeuSerLysCysGlyProGlyPheGlyVa 135
                                                                                                                                                                                                                                                                                                                                              SGTTICTITCIAAGAGAAAACGAGIGIGIGICTOTGIAGIAGIAACIGIAAG 558
                                                                                                                                                                                                                                                                                                                                                                                                         ilyThrPhe. ...SerAspIhrThrSerIhrAspVal*ysArd 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HisArdLeCysSerIleLeuAlaIleProflyAshAlaSerThrAs 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FGAAAAAAAGGGGGGGGCTTGAAGGAACTACTACTAAGGCCCTGGCCC 805
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Percent Similarity:
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A. Crass-references: CR-SC3368 NID-g235649
A. Note: Sequence extracted from NCB1 backbone (NCB1N:63368, NCB1P:63371)
B. Heller, B. A. Song, K. Glasch, M. A. Fisher, W. H.; Chang, D.; Fingeld, G. M. Proc. Natl. Acad. Sci. U.S.A. 87, 6151-6155, 1990
A.TILLE: Complexementary DNA Calculus of a receptor for times nevices factor and demonstral A. Reference number: A36007, MUID:90349572
A:Title: A receptor for tumor necrosis factor defines an unusual family of cellular and
A:Reference number: A35356; MUD:902knβ39
                                                                                                                                                                                                   A:Molecule type: mRNA

A:Molecule type: mRNA

A:Residues: 1.461 (SMI)>

A:Cross-references: 38:M32315; N:D:g189185; PIDN:AAA59929.1; P:D.g189186

R:K.Jan., 1. Ricker, N. T. Baker, S. 1. Schwartz, P. F., King, M.W., Haie, K.K., Squitus, Proc. Natl. Acad. Sci. U.S.A. 87, 8331-8335, 1990

A:Tille. Nat Second Lumor necrosis factor immer: qene product can shed a naturally occur

A:Reterence number: A36475; MOID:91045991
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R:Dembic, Z.: Loetscher, H.; Gubler, H.; Pan, Y.C., Lahm, H.W.; Gentz, R.; Brockhaus, M.
Cytoking 2, 231-237, 1990
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A.Residues: 116-140, Pv.142-195, Rv.197-3£2, Tv.364-461 <HEL>
A.Cross-ferences: 116-140, Pv.142-195, Rv.197-3£2, Tv.364-461 <HEL>
A.Cross-ferences: 116-140, Pv.142-195, Rv.197-3£1: PIDN-AAA42£2 1: PID-g4497£2
F.Loottscher, H., Schidesper, E.J.; Indum, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus, M.
J. Hiol. Chem. 265, 20131-20138, 1990
A.Tifler, Purification and partial amino acid sequence analysis of two distinct tumor ned
A.Rerespence number: A24666
A.Rerespion: A24666
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A:IIIle: Two tumor necrosis lactor-binding proteins purified from human urine. Evidence A:Reference number: A:5010; MUID:90110215
A:Accession: B:5010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Affitle: Two human TNF receptors have similar extracellular, but distinct intracellular, A:Reference number: A48416; MUID:91370690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CSuperfamily: humor nectors is factor receptor type 2. NOF receptor repeat homology conversals duplication, elecation, receptor, trensmembrane protein principles of the proposition of the product of th
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A)Status (pellatour, trunslate) from Hylematherman Mondecule type: DNA
A)Residues: 1-37 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A:Status: preliminary
A:Molecule type: protein
A:Residues: 23-40;65-69;136-141-300-306 <108>
A:Encolmann, H.: Novick, D.; Wallach, D.
J. Biol. Chem. 265, 1531-1536, 1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the list of introns is incomplete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: mRNA
A;Pesidues: 1-195,'R',197-461 -KOH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Accession: A48416
A;Status: preliminary
A;Molecule type: mRNA; protein
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A:Molecule type: protein
A:Residues: 27-31 <ENGS
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Gene 150, 381 386, 1994
                                                                                                                                                                                      A;Status: preliminary
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                                                                                                                                  A;Accession: A35356
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F;171,193/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          224 CCCCCCAGCATACCCACTGCAGGGGTTCTCACCCGGCTCCTTCACCCCT 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             371 TOTGTGGCTGCAGGAAGAACCAGTACCGGCATTAITGGAGTGAAAACTT 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         421 TECAGEGERICANTEGRACIOTOTOTOTOTATEGGACCGTGCACCTCTC 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               124 AGTGTGTGTCCCCAAGGAAATAIATGCACCCTCAAAATAATTGGATTTG 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    174 CIGIACCAASIGS AAAAAAAAAACIAATIGIALAAIGACISICCAGGCC 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                274 TCAGAAAACCATACTCAGACTGCTCACACTGCCCCCAAATGCCGAAA 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86 LouTrpAsnTrpValProCluCysLouSerCysClySerArgCysSerSe 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117 leGysThrCysArgProGly......TrpTyrGysAlaLeu 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                139 .....ProLeuArgLysCysArgProGlyPheGlyV 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGAGAAAAAGAGTGTGTCTCTGTAGTAACTGT... 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                149 alAlaArgFroslyThrSluThrSerAspValValCysEysFroCysAla 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          166 ProGlyThrPheSerAshThrThrSerSerThrAspIlcCysArgProHi 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F92 FAGATTGAGAATHTTAAGAGTATTGAGGGTAGGGTAGTGTGT 640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   182 sGlnIleCysAsnVal.....ValAlaI 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          641 IGCCCCIGGICALITICITIOGICITIGCCTTITATCCCTCCTCCTTCATT 690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    691 GOTTTAATGTAFCGCFACCAACGGTGGAAGTCCAAGCTCTACFCCATTGT 740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          741 ITSTEGGRAATSSANASTSSANAAASNAGGGGGAGSTIGAAGGAACIASTA 790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   791 CTAAGGGGGGGGGGGAAAGGGAAGGTTCAGTGGGAGTGCAGGGTTCACC 840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       192 .......GlyAsnAlaSerMetAspAlaVa 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38 SerThrCysArgLeuArgGluTyr...TyrAspGlnThrAlaGlnMetCy 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53 stysSerLystysSerProflyGlnHisAlaLycValPhetysThr...L 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 https://www.nysthrvalCysAspSerCysGluAspSerThrTyrThrGln 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAGAAAAGCCTGGAAGTGCAAAGTGCGCCCC
F)164-201/Nomain: NCF receptor repeat homology :NC4> P)262-279/Nomain: transmembrane #status predicted <FMN> F)280-461/Domain: intracellular #status predicted <INT>
                                                                                                                                                                                                                                                 L.074 Gaps: 21 45:024 Percent Identity: 24.645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seq 1/1 to: A35356 trom: 1 to: 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             199 10; sThrSerThrSerPro.
                                                                                                                                                                                                                                                         Quality: 204.00
Ratio: 1.074
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US-09-525-998A-1 x A35356
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	US-09-525-994A-1 x 60VZML Aliqu seq 1/1 to: 00VZML from: 1 to: 326	40 GTGCTGCTGAAGCTGTTGGTGGAAATATACOCTCAAGGGTAATTGGAACT 89 ::: 1 1 1 1 1 1 1 1 1 1 1 1	90 GGTCCCCAACAAGAAAAAAAAAAAAAAAAAAAAAAAAAA	140 GAAAATATATOGACSCICAAAATAATTGGTGTAYCAAGTGCCA; 189 ::	190 AAAGGAACCTACTTGTACAATGACTGTGGGGGGGGGGGG	240 CIGCAGGGAGIGIGASAGCGGGCCITCACGGCGTCAGAAAAACGGGGA 289 	GAGACTOGCTCAGCTGCTCCAAATOGCGAAATGGAAATGGGTGAGTG TELETTH HTT	GAGATOTOTTGCACAGTGGACGGGACACCGTGGGTGGGTGGGAAA 	GAACCADIA". (11) aOlyAsniyrOysLeuLeuLysOlyOlnOluGlyOysArqIleOysAlaP	396	142 GlyaspvallesiCysthrlysCysProArditytEstashava 158	420 TTTCCAGLGAATIGCAGGCCGGCATCAATGGCACCSIGCACC 466 1151 TST 15 TST 17	TCTCCTGCCAGGAAAAACAGAACAGCGTGCAGGTATCGCTGCTAGGAGGTTCCTGCTGCTAGGAGAACAGAACAGCGTGTAGGAGGTTTCCTGTTTTTTTT	517 IIIOIAAAAAAAAGIGIGIGIGIGIGIAAGIAAGIAAAAAAAA	567 GOMGLOPAGGARGITGIGGGTAGGGARIDADARIGITA 607 1::1:1 204 uAshilatarAspOyrAspProValtheHistbrGlotyrTyrGlythrS 221	608 AGGGACHGARRACHAGGG 627 ::III:::III ::IIII :::::::::::::::::::	seq_indme. pill.CHOUOK	seq_documentation_block: nerve_growth factor receptor, low_affinity_precausor - chicker. N;Alternate names: NSF receptor C;Species: Galbus aallus (chicken) C.Saeries: Ab Sep.) for assequence_textsion to seption attext_character 10 Sep.1999
	841 CCCACCTGGGCTTCAGTCCCGTGCCAGTTCCACCTTCACCTCCAG 887 :::::::::::::::::::::::::::::::::::	CTCCACCTATACCCOC 6616ACTGTC 91 (11) 111 111 111 111 111 111 111 111 1	914 CTAACTITGGGGGTCCCGGCAGAGGTGGCACACACCCIAICAGGGGCT 963 :::	GACCCATCCTTGCGACAGCCCTCGCACCCATCCCATCCC	1014 TCANAANATOPENANTANINANTONINANANANINANANANTANINANINANINANINANINAN	1063 A		1148 ACGAGALCGALCGGCIGGAGTTGTAGATGGGCIGCCIGCGGGGGGGGGGGG	1195 GCGCAATACAGATAGTAGACATAGAAAAGAGAAAAAAAA 1244 ::	1245 GANTAMARTIGNAGNIGRIGGGARGTIGGGGGACANGGACTINT GG 1294 	1295 GCTGCCTGGAGAAT 1310 :	eq_name: pirl:GUVZML	<pre>seq_documentation_block: 2 protein · myxema virus (strain Lausanne) ;Species: myxema virus ;Species: myxema virus ;Date: 31 Dec 1992 #sequence_revision 31-Dec-1992 #text_charge 18-Jun-1999 **Accession: #A6566</pre>	According Marken, J.L.; Schreiber, M.; McLadden, G. Virology 184, 370-382, 1991 Walitle Mysma Virus Captusas a secteted protein with hemelogy to the tumor new	A.Accession: A4056 A.Molecule type: DNA A.Residues: 1-326 (4DPA) A.Crossiches: 1-326 (4DPA)) Superfamily, myxoma virus 12 protein, NGF receptor repeat homology () Reywords: glycoprotein () Reywords: glycoprotein () Reywords: glycoprotein repeat hearly note.	7,000 1477DOMMAIN: Now Tetrphon Tepral HOMOTONY SN032 7:66,181,205,238/Binding site, carbobydrate (Asn.) (covalent) #status predicted	ilignment_scores: Quality: 200 00 Longth: 240 Ratio: 1.695 Gaps: 10 Percent Similarity: 49.167 Fercent Identity: 25.833

crclys 113

CICICICC 471

1111100 424

PhePro 129

ACTGIA 556

lecysd 163

AATGTT 606

yrhrPh 146

TTTCTT

172

CATITIT 656

185

ALCGCI 706

185 756

.

eThrAr 205

TOGACA

AlaAsp 219

ACCTCC 885 4G17Th 236

GCTTCA 856

425 alValV 254 AICAGG 958

	200 ProGlu	857 GPCCCGFGCCCAGPTCCACCTTC 1:: 220 LieValThrThrValMetGlySerSerGlnProValValSerAr	886 AGCHCPARTHARACHARACHGARAITGAARTHAGAGG 111 111111 236 rAlaAspAsnicuilebrovalTyrcysScriicicualaAlaV 926 926 - GTCHCPASTAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGA		959 GGCTGACCCCA Production of the Company of the Co	uclyclutyst	1072 AracharachidangaAndrachidangananangangggggggggggggggggggggggggg	4	
A:Reference number: J00006; MUID:90166579 A.Accession: J00006 A.Accession: J00006 A.Accession: J00006 A.Experimental source: embryonic chick brain A.Experimental source: and developmental expression of the chicken NGF Leceptor. A.Accession: A6054 A.Stelence number: A60504, MUID:90152140 A.Accession: A6054 A.Stelence number: A60504, MUID:90152140 A.Stelence number: A60504, MUID:90152140 A.Stelence number: A60504, MUID:90152140 A.Stelence number: A60504, MUID:90152140 A.Stelence number: A60504 A.Stelence number: A60	alignment_scores:	alignment_block: US-09-525-998A-1 x JN0006 Alian sea 1/1 to: JN0006 from: 1 to: 416	naactertogroggaarayacceteagger 	81 TATTGGACTCCTCACCTAGGGGAGAACAGAGATAGTGTCT :	131 GTCCCCAAGGAAATATATCCACCTCAAAATAATTCGATTTGCTGTACC 1 1 1 1 1 1 1 1 1	181 AAGTGCCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGCA :	278 AAAACCACTCAGACACTGAGCTGCAAATGCCGAAAGGAAATG	328 GGTCAGGTGGAGATGTCTT, TGCAGAGTGGAGCGGGAGACTGTG 37 [1] 11 11 11 11 11 11 11	

CCCAAC 1008

Lyscin 269

286

rProGl

ACAGGG 1033

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GCGC.. 1110

Prollys 319

GGAAGG 1117

rLysGl 333

CTGGAG 1167

rpArgG 350

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350 InternateClyCluteuclyTyThysStaAspteutleAsp363	322 CA
1168 CTGPAGAAPTGGGTTGGTTGGTGGAAAAAAAAAAAAAAAA	Time to the control of the control o
GCTGGGGAACTGGAACGGGAACAAAAAAAAAAAAAAAAA	; — C
uLeuAlaAspTrpSerAlaLysGluThrAlaThrLeuAspA	
389 Tatteut.cuVaTATatteuArgttysTTedInArgGTyAsp 401	472 IG
1309 ATCGAGGAGGGTT 1223 	: 44 80 00 10 00
seq_name: pir2:H43692	
eq_documentation_block:	572 60
12 profesa rabbit fibroma virus. Shope fibroma virus	941
Juater in September 1999 S. Accession: B43692 R. Ubion, C. J. Delange, A. M.; McPadden, G.	616 GA
Virology 160, 20-30, 1987 ArTitles Tumoriquenic poxylituses: genomic organization and DNA sequence of the telomeric A.Reference number: A43692, MJD:87321103	162 GI
AyAcression: 843692 AyStatus: preliminary	168
N. Posidies: 1-32:	716.90
A.Cross-references: GB:M14433 [:Superimaly, myxema virus II protein, NCF receptor repeat homology	173 41
F104-105/Domain: NGF receptor repeat homology <ng2> F1104-147/Abenain: NGF receptor repeat homology <ng3></ng3></ng2>	45 33L
	181
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CAGATA	C:Date: 19. C:Accession
17 pAspValProTyxSerSerAsnSlnGl7Lys 27	E, Watasake J. Immunol.
125 GIGIGICOCCAAGGAAAATATATCCAGCCCAAAAATAATCCGATTTGC 174	Arrithe, Th
28CjsCijGljHisAspijrCluijsAspCljheuCjs 39	A, Accession
身	A;Status: p A,Molecule
40 CysAlaSerCysHisProGlyPheTyrAlaSerArgLenCys OlyPr 55	A:Residues: A,Cross ret
225 GCCCCAGCATACCSACTICCASCSACTICACACCCCTICCTTTCACCCCTT 274	A.Experimen A.Exte. seq
	RyAdachi, M Proc. Matl.
275 CAGAAAACGCCCGAGACGCGCGCGGGCCCGAAATGCGGGAAAG 321	A;Title: Ab A;Reference
	A;Accession A;Status: r

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Mus musculus (fource mouse)

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Fakandasa, B., Brandas, C.E., Itch, N., Yonebara, S., Copeland, N.G.; Jenki

148, 1274-1279, 1992

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Appende vertaated from Noble Lackbook (N'BENNEELA44, NCBEP-81545)

ALL Wernbacke Poblanga, R.; Nagata, S.

A.C. Wernbacke Poblanga, R.; Nagata, S.

A.C. Acad, Sol. U.S.A. 90, 1754, 1754, 1994

Perfant transcription caused by the insertion of an early transposable elem-

annihet: A47254; MOIDCHSIN9576
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Length:	813
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78 GGTTATTGGATCCTCACCTAGGGGAAACAAGAAA	Biochem. A.Title.
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119 GAGATAGIGIGIGIPATOPOPAAAAAATATOPOPOPOAAATAATAATOR 168	A;Molecul A;Residue A;Cross-r
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, K.; Wakatsuki, T.; Yamamoto, M.
Biophys. Res. Commun. 198, 646-674, 1994
A vaitant mENA species encoding a 12-noused from of Fas antiqen in the rat. 1
nor number: JC2395; MUD:94128114
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Nontal source: thymus
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Hental source: liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     is Rattus norvegicus (Norway rat)
20 Feb 1935 #sequence_revision 20 Feb 1995 #text_change 05 Nov-1999
Don. JC2395, PC2246
                            TGSANGTODAAGOTOTAGTOGATTGTTTGTTGTGGGAAATGGAGAGGTGAA 762
                                                                                                                                                                  AAAGAGGGGAGGTTGAAGGAAGTAGTACTAAGGCCCCTTGGCCCCAAAGCC 812
TEGOCITYIATGCCFCCTCTTCATTGGITAATGIATCGCTACCAACGG, 714
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ss: 1-62, 'PPT' <K12>
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216	TCCACCCCGGGCCASCATACGGAGGAGGGGGGGGGGGGGG	2 2
263	CCTICACCGCIICASAAAAAACICCAGAACACGGGGGGGGGGG	7 0
313	TGCCGAAAGGAAATGGGTCAGGTGGAGATCTGTTCTTCTGCACCG 36	
103	(1) ::: ::: CysAspGluGlyHisGlyLeuGluValGluThrAsacysThrArgThrGl 11	6.
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114	nasnihilysCysArqCyslysCluAsn12	8
413	AAAACCITTICCAGISCIICAAIIGCAGCCICIGCCICAAIGGGAGCGIG 46	2.5
129	Phetyrcyssnhlettil	9
463	CACCHICTCCTGCCAGGAGAACAGAACACGTGTGCACCTGCCATGCAGG 51	7
136	13	9
513	TITCTITCIAAGAGAAACGAGIGIGICTCCTGTAGTAACIGTA 55	9.
137	AspHisCysTyrHisCysTytRisCysTyleuG 14	89
557		33
148	luAspileLeuGluProCysThrArgThrSerAsn 15	63
404	01114A0000A0116A004A017A007A0140140140140140140140140140140140140140	83
160	ThrLysCysLysLysGlnSerSerAsnTyrLysLeuLeuTrpLeuLeuIl 176	9,
654	TITCITIGGICITIGCCITITATCCCT	3
176	eleuproclyleuAlalieleuphevalpheileTyrlysA 19	0
704	GCTACCAACGGTGGAAGTCC 72	63
190	ITTPLE I	9(
724	AAGCTCTAC	
206	odluserValProMetAsqValSerAspValAsnLeuAsnL	

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